

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1985	100.0	389	2	O59096	O59096 pyrococcus
2	1872	94.3	389	1	AAT_PYRAB	Q9v0l2 pyrococcus
3	1784	89.9	389	2	Q8U1F5	Q8ulf5 pyrococcus
4	1058	53.3	390	2	Q9UZ63	Q9uz63 pyrococcus
5	1019	51.3	390	2	Q8U3E6	Q8u3e6 pyrococcus
6	1014	51.1	391	1	AAT_PYRHO	O58489 pyrococcus
7	1013	51.0	388	2	Q8RCV4	Q8rcv4 thermoanaer
8	973.5	49.0	388	2	Q8R7H1	Q8r7h1 thermoanaer
9	935.5	47.1	396	2	Q6HC04	Q6hc04 bacillus th
10	935.5	47.1	396	2	Q81K72	Q81k72 bacillus an
11	935.5	47.1	396	2	AAT34262	Aat34262 bacillus
12	934.5	47.1	396	2	Q816F8	Q816f8 bacillus ce
13	931.5	46.9	396	2	Q72YI1	Q72yi1 bacillus ce
14	931.5	46.9	396	2	AAS43941	Aas43941 bacillus
15	897.5	45.2	393	2	Q9K7L1	Q9k7l1 bacillus ha

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1985	100.0	389	2	E71009	probable aromatic-
2	1872	94.3	389	2	B75122	probable aromatic-
3	1058	53.3	390	2	G75037	probable aromatic-
4	1014	51.1	391	2	E71125	probable aromatic-
5	897.5	45.2	393	2	F84068	aspartate aminotra
6	866	43.6	374	2	G69119	probable aspartate
7	845.5	42.6	390	2	F69452	probable aspartate
8	804.5	40.5	379	2	A69516	probable aspartate
9	795	40.1	394	2	A70469	aspartate transami
10	789.5	39.8	386	2	H96945	PLP-dependent amin
11	782.5	39.4	388	2	AE2412	aspartate aminotra
12	766	38.6	375	2	A64300	aspartate transami

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length	Length			
1	389	100.0	389	3	AA77535	Aay77535	Pyrococcus
2	389	100.0	389	3	AA85619	Aay85619	Thermoplasma
3	389	100.0	389	5	ABG31066	Abg31066	Aromatic
4	49	12.6	389	4	AAB96229	Aab96229	Putative
5	35	9.0	392	8	ADN47893	Adn47893	Thermoplasma
6	15	3.9	390	4	AAB96556	Aab96556	Putative
7	14	3.6	392	8	ADN47966	Adn47966	Thermoplasma
8	12	3.1	369	7	ADE12735	Ade12735	L. rhamnosus
9	12	3.1	391	5	AAE20095	Aae20095	Lactobacillus
10	12	3.1	418	6	ADA33238	Ada33238	Acinetobacter

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	795	40.1	394	2	US-08-646-590B-40	Sequence 40, Appl	
2	795	40.1	394	3	US-09-412-184-40	Sequence 40, Appl	
3	785	39.5	398	2	US-08-599-171A-29	Sequence 29, Appl	
4	785	39.5	398	2	US-08-646-590B-29	Sequence 29, Appl	
5	785	39.5	398	3	US-09-069-226-29	Sequence 29, Appl	
6	785	39.5	398	3	US-09-412-184-29	Sequence 29, Appl	
7	704	35.5	389	4	US-09-134-000C-3706	Sequence 3706, Ap	
8	687	34.6	418	4	US-09-328-352-4525	Sequence 4525, Ap	
9	672	33.9	399	4	US-09-134-000C-6422	Sequence 6422, Ap	
10	665	33.5	390	4	US-09-107-532A-5233	Sequence 5233, Ap	
11	629.5	31.7	411	4	US-09-107-532A-4942	Sequence 4942, Ap	
12	619	31.2	385	3	US-09-413-814-7	Sequence 7, Appli	
13	617.5	31.1	395	4	US-09-583-110-3337	Sequence 3337, Ap	
14	597.5	30.1	390	4	US-09-724-623-67	Sequence 67, Appl	
15	589	29.7	410	4	US-09-252-991A-33110	Sequence 33110, A	
16	587	29.6	395	3	US-09-134-001C-3723	Sequence 3723, Ap	
17	569.5	28.7	369	4	US-09-724-623-66	Sequence 66, Appl	

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	389	100.0	389	9	US-09-967-645-1	Sequence 1, Appli
2	389	100.0	389	14	US-10-369-493-1298	Sequence 1298, Ap
3	389	100.0	389	14	US-10-369-493-20364	Sequence 20364, A
4	389	100.0	389	16	US-10-810-440-1	Sequence 1, Appli
5	49	12.6	389	14	US-10-369-493-21601	Sequence 21601, A
6	17	4.4	312	15	US-10-424-599-249656	Sequence 249656,

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	12	3.1	369	4	US-09-724-623-66	Sequence 66, Appl
2	12	3.1	418	4	US-09-328-352-4525	Sequence 4525, Ap
3	10	2.6	394	2	US-08-646-590B-40	Sequence 40, Appl
4	10	2.6	394	3	US-09-412-184-40	Sequence 40, Appl
5	9	2.3	216	3	US-09-134-001C-3618	Sequence 3618, Ap
6	8	2.1	295	4	US-09-583-110-4171	Sequence 4171, Ap
7	8	2.1	303	4	US-09-252-991A-27331	Sequence 27331, A
8	8	2.1	398	2	US-08-599-171A-29	Sequence 29, Appl
9	8	2.1	398	2	US-08-646-590B-29	Sequence 29, Appl
10	8	2.1	398	3	US-09-069-226-29	Sequence 29, Appl
11	8	2.1	398	3	US-09-412-184-29	Sequence 29, Appl
12	8	2.1	440	4	US-09-252-991A-22913	Sequence 22913, A
13	8	2.1	515	4	US-09-134-000C-4651	Sequence 4651, Ap
14	7	1.8	33	1	US-08-781-020-15	Sequence 15, Appl

RESULT 2

US-10-369-493-1298

; Sequence 1298, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 1298

; LENGTH: 389

; TYPE: PRT

; ORGANISM: Pyrococcus horikoshii

US-10-369-493-1298

Query Match 100.0%; Score 389; DB 14; Length 389;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALSDRLELVSASEIRKLF	DIAAGMKDVISLGIGEPD	FDT	PQHIKEYAKEALDKGLTHY	60
Db	1	MALSDRLELVSASEIRKLF	DIAAGMKDVISLGIGEPD	FDT	PQHIKEYAKEALDKGLTHY	60
Qy	61	PNIGLLELREAI	AEKLLKQNGIEADPKTEI	MVLLGANQAF	LMGLSAFLKDGEEVLIPT	120
Db	61	PNIGLLELREAI	AEKLLKQNGIEADPKTEI	MVLLGANQAF	LMGLSAFLKDGEEVLIPT	120
Qy	121	FVSYAPAVILAGGK	PVEVPTYEEDEFRLN	VDLKKYVTDKTRALI	INSPCNPTGAVLTKK	180
Db	121	FVSYAPAVILAGGK	PVEVPTYEEDEFRLN	VDLKKYVTDKTRALI	INSPCNPTGAVLTKK	180
Qy	181	DLEEIADFVVEHDL	LIVISDEVYEHFIYDD	DARHYSIASLDGM	FERTITVNGFSKTFAM	240
Db	181	DLEEIADFVVEHDL	LIVISDEVYEHFIYDD	DARHYSIASLDGM	FERTITVNGFSKTFAM	240
Qy	241	RLGFVAAPSWIIE	RMVKFQMYNATCPVT	FIQYAAAKALKDERS	SWKAVEEMRKEYDRR	300
Db	241	RLGFVAAPSWIIE	RMVKFQMYNATCPVT	FIQYAAAKALKDERS	SWKAVEEMRKEYDRR	300
Qy	301	VWKRLNEMGLPTV	KPKGAFYIFPRIRD	TGLTSKKFSEML	LKEARVAVVPGSAFG	360
Db	301	VWKRLNEMGLPTV	KPKGAFYIFPRIRD	TGLTSKKFSEML	LKEARVAVVPGSAFG	360
Qy	361	VRISYATAYEKL	EEAMDRMERVLKER	KL		389
Db	361	VRISYATAYEKL	EEAMDRMERVLKER	KL		389

RESULT 3

US-10-369-493-20364

; Sequence 20364, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 20364

; LENGTH: 389

; TYPE: PRT

; ORGANISM: Pyrococcus horikoshii

US-10-369-493-20364

Query Match 100.0%; Score 389; DB 14; Length 389;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALSDRLELVSASEIRKLF	DIAAGMKDVISLGIGEPD	FDT	PQHIKEYAKEALDKGLTHY	60
Db	1	MALSDRLELVSASEIRKLF	DIAAGMKDVISLGIGEPD	FDT	PQHIKEYAKEALDKGLTHY	60
Qy	61	PNIGLLELREAI	AEKLLKKQNGIEADPKTE	IMVLLGANQAF	LMGLSAFLKDGEEVLIPT	120
Db	61	PNIGLLELREAI	AEKLLKKQNGIEADPKTE	IMVLLGANQAF	LMGLSAFLKDGEEVLIPT	120
Qy	121	FVSYP	AVILAGGKPV	EVP	TYEEDEFRLNVDELKKYVTDKTRALI	180
Db	121	FVSYP	AVILAGGKPV	EVP	TYEEDEFRLNVDELKKYVTDKTRALI	180
Qy	181	DLEEI	ADVFVVEHDLIVISDEV	YEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGW	240	
Db	181	DLEEI	ADVFVVEHDLIVISDEV	YEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGW	240	
Qy	241	RLGFVAAPSWII	ERMVKFQMYNATCPVT	FIQYAAAKALKDERSWKAVEEMRKEYD	RRRKL	300
Db	241	RLGFVAAPSWII	ERMVKFQMYNATCPVT	FIQYAAAKALKDERSWKAVEEMRKEYD	RRRKL	300
Qy	301	VWKRLNEMGLPTV	KPKGAFYIFPRIRD	TGLTSKKFSELM	LKEARVAVVPGSAFGKAGEGY	360
Db	301	VWKRLNEMGLPTV	KPKGAFYIFPRIRD	TGLTSKKFSELM	LKEARVAVVPGSAFGKAGEGY	360
Qy	361	VRISYATAYE	KLEEAMDRMERVL	KERKLV	389	
Db	361	VRISYATAYE	KLEEAMDRMERVL	KERKLV	389	